Amendments to the Specification:

Please replace the paragraph beginning on page 2, line 2 and ending on page 3, line 1, with the following amended paragraph:

The invention will be described in closer detail in the following, with support of the enclosed examples and figures, in which

Fig. 1 shows the adherence values as a function of fibrinogen coating concentration for the *S. epidermidis* strains 2, 19 and JW27 (Example 1A),

Fig. 2 shows percent inhibition for antibodies against fibrinogen, compared to antibodies against fibronectin (Example 1B),

Fig. 3 shows percent inhibition as a function of competing fibrinogen concentration (Example 1C),

Fig. 4 shows the protease sensitivity of adherence to fibrinogen (Example 1D),

Fig. 5 shows the inhibition of adherence by LiCl extract (Example 1E),

Figures 6A-6E show the complete nucleotide sequence of the *fig* gene from *S. epidermidis* strain HB and the deduced amino acid sequence of the encoded protein ~~(SEQ ID NO:14)~~ (SEQ ID NOS:14 and 15). A putative ribosomal binding site (RBS) is underlined and a possible transcription termination hairpin loop is double underlined. A putative signal sequence (S) is indicated with an arrow and the translational stop codon with an asterix. The start of the non-repetitive N-terminal region called A, harbouring the fibrinogen binding activity is indicated by an arrow. R indicates the highly repetitive region. The 5 amino acid motif involved in cell wall anchoring is indicated in bold characters and the membrane-spanning region is marked M (Example 3),

Fig. 7 shows a schematic drawing comparing the fibrinogen binding protein FIG of *S. epidermis* and the clumping factor (ClfA) of *S. aureus*. The similarity, (%), of corresponding regions in the proteins is indicated in the figure between the two protein bars. S is the signal sequence; A, the non-repetitive region harbouring the fibrinogen binding activity; R, the diamino acid residue repeat region; W the region proposed to be

involved in cell wall anchoring and M, the transmembrane domain. The numbers indicated refer to the amino acid positions in respective proteins as shown in figures 6A-6E and 7 and in reference (McDevitt et al., 1994) (Example 3),

Fig. 8 shows how GST-FIG fusion protein is captured to fibrinogen in a dose dependent way (Example 10),

Fig. 9 shows the decrease of bacterial binding as a function of GST-FIG fusion protein, GST or FIG (Example 11),

Fig. 10 shows the relative adherence as function of serum dilution for two pre immune sera and a serum against GST-FIG and FIG, respectively (Example 12), and

Fig. 11 shows the relative bacterial adherence as a function of serum dilution for, on one hand, pre immune serum and, on the other hand, serum against GST-FIG (Example 12).

Please add the following new paragraphs after the last line of text on page 21 of the application (i.e., at the end of the specification immediately before the claims):

--The nucleotide sequence shown in the above SEQ ID NO: 10 encodes a protein which contains 593 amino acids. SEQ ID NO: 11 is the amino acid sequence of this protein.

SEQ ID NO: 12 is the nucleotide sequence containing 1746 nitrogenous bases which code for the 582 amino acid FIG protein. As discussed above, the 582 amino acid FIG protein is encoded by the insert of pSE100. The nucleotide sequence of SEQ ID NO: 12 corresponds to bases 255-2000 shown in figures 6A-6E.

SEQ ID NO: 13 is the deduced amino acid sequence encoded by SEQ ID NO: 12. Thus SEQ ID NO: 13 is the 582 amino acid sequence of the FIG protein and thereby corresponds to amino acids 75-656 of the sequence depicted in figures 6A-6E. In other words SEQ ID NO: 13 is the amino acid sequence of SEQ ID NO: 11 without the Pel leader sequence and the Myc tail.

SEQ ID NO: 15 is the deduced amino acid sequence encoded by SEQ ID NO: 14, i.e., the amino acid sequence shown in figures 6A-6E.--